Amendments to the Specification:

Please replace the paragraph on page 3, lines 21-30, with the following amended paragraph:

A few years ago immunophilins from plant extracts from *Vicia faba* were isolated via their affinity to FK506 and cyclosporinA (Luan et al., 1994, Proc. Natl. Acad. Sci. USA 91: 984-988). During this process an FKBP12 was isolated, which showed high sequence homology to FKBP12 from yeast and animals (between 47%-51% amino acid sequence identity). *In vitro* this FKBP12 from *Vicia faba* showed, however, little affinity to calcineurin, and expressed in yeast it did not mediate the effect of FK506 and rapamycin (Xu et al., 1998, Plant J. 15: 511-519). In *Vicia faba* injected FK506 could only inhibit a calcium dependent regulation of ~~calium~~ calcium channels in guard cells, if human FKBP12 was also applied at the same time (Luan et al., 1993, Proc. Natl. Acad. Sci. USA 90: 2202-2206), which is a hint to the presence of a FKBP12-FK506 signal transduction chain in plant cells, without having an endogenous receptor for FK506.

Please replace the paragraph on page 6, lines 23-28, with the following amended paragraph:

The term „hybridisation" or „hybridising" as used herein, means stringent and less stringent conditions; see. Sambrook et al., Molecular Cloning, Cold Spring Harbour Laboratory (1989), ISBN 0-87969-309-6. An example of stringent hybridisation conditions is: hybridisation in 4 x SSC at 65° C (alternative in 50% Formamid and 4 X SSC [[bei]] at 42° C), followed by several washing steps in 0,1 x SSC at 65° C for altogether one hour. An example for less stringent hybridisation conditions is hybridisation in 4 x SSC at 37° C, followed by several washing steps in 1 x SSC at room temperature.

Please replace the paragraph on page 9, lines 7-20, with the following amended paragraph:

The present invention refers to nucleic acid sequences from a plant genome, particularly

preferred from *Arabidopsis thaliana*, *Zea mays* or *Lycopersicon esculentum* that contain the coding region of an FKBP-like (FK506 binding protein) gene (twisted dwarf), whose activity controls the shaping of the entire architecture of the plant, in particular cell growth, growth orientation, degree of branching, etc. The discontinuation of these activities, for instance due to mutation or deletion in a plant genome leads to a change in the entire architecture of the plant through reduction of cell growth, disorientation of the growth of all organs above and below ground, reduction of branching of the stem, changes in the reaction towards brassinosteroids and their precursors and derivatives and the change in the reaction of the roots to gravitropism resulting in the change of ~~ethylen~~ ethylene production and ethylene induced signal transmission. The nucleic acid sequence according to the invention can be inserted into a vector, which also comprises one or more regulatory elements that control the transcription and/or translation of the nucleic acid sequence according to the invention. Further, the invention refers to vectors, for instance plasmids, and host cells, such as yeasts and bacteria including the nucleic acid sequence according to the invention.

Please replace the paragraph on page 14, lines 23-30, with the following amended paragraph:

In order to investigate if the root gravitropism of the twisted dwarf mutant was corrected by the effect of the phytohormone ~~ethylen~~ ethylene, the influence of inhibitors of ethylene biosynthesis and of inhibitors of ethylene response on the root gravitropism of twisted dwarf and wild-type seedlings was studied. The same experiment described above was conducted but with an addition of silver nitrate, an inhibitor of the ethylene effect, in the Arabidopsis medium. A concentration of 1 μM silver nitrate in the growth medium, and 10 ppm ethylene in the growth chamber led to increased agravitropic growth in the roots of the twisted dwarf mutant. This effect was not found in wild-type plants. Amino ethoxyvinylglycin (AVG), which inhibits the endogenous ethylene biosynthesis, led in a concentration of 1 μM to only

Please replace the paragraph on page 17, lines 17-30, with the following amended paragraph:

With a positive colony 150 ml antibiotics containing YEB medium were inoculated and shaken for 2 days at 28°C. With 10-15 ml of this culture 500 ml antibiotics containing YEB-medium were inoculated. This culture was incubated over night at 28°C on the shaker and pelleted the next day for 15 min. at 4,000 rpm. The sedimented bacteria were taken up in infiltration medium. The concentration of the suspension was determined by turbidity measurement and set at a OD600 (optical density) between 0,8 and 1,2. 400 ml beakers filled with Agrobacteria suspension were put into a vacuum exicator. Pots with Arabidopsis plants were placed upside-down on the beakers so that the inflorescences of the plants reached into the Agrobacteria suspension. A ~~vakuum~~ vacuum of 10-30 mbar was applied for 15 min and then the vacuum exicator was quickly aired. A bacteria suspension was employed for as many as four continuous infiltrations. Afterwards, the plants were kept further under long-day conditions (16 hours light/8 hours darkness) until the siliques were ripe. The 10 plants in one pot were put in two bags (2 pools) of 5 plants each to collect the seeds when the oldest siliques were ripe. The well-dried seeds could be directly sewn on soil for a selection with BASTA® (Aventis CropScience, S.A., Lyon, Frankreich)

Please replace the paragraph on page 18, lines 9-11, with the following amended paragraph:

Isolation of the FKBP-like twisted dwarf gene from T-DNA tagged insertion lines of *Arabidopsis thaliana* by means of plasmid rescue and the isolation of [[von]] the full length cDNA and genomic clones from gene libraries.

Please replace the paragraph on page 21, lines 24-30, with the following amended paragraph:

The obtained PCR product (SEQ [[IC]] ID NO:4) was cloned into the vector pGEM-T easy® (Promega) and sequenced by the chain termination method according to Sanger. By means of the sequences of the EST-clones AW038756, AW1895686, AW441601, AW222544 from tomato (*Lycopersicon esculentum*) (GenBank online, Release >115), which was found with the aid of the similarity logarithm BLAST (Basic Local Alignment

Search Tool, Altschul et al., Journal of Molecular Biology 215, 403-410 (1990) (tblastn, cutoff for P value: $6e^{-26}$, Matrix: Blosum 62, Gap existence cost: 11, Per residue gap cost:1) with the amino acid sequence of the Arabidopsis TWD protein, a cDNA Contig over

Please replace the paragraph on page 22, lines 1-6, with the following amended paragraph:

altogether 1142 base pairs could be assembled (TomTWDContig; SEQ ID NO:5). The area of sequence overlaps comprises the nucleotide positions 1 to 95 from TomTWD [[mit]] with AW441601 and 121 to 140 from TomTWD with AW222544. The translation of the longest open reading frame of the nucleotide sequence of TomTWD Contig in amino acids results in a continuous peptid (TTP) which is 320 amino acids in length. The identity to the TWD protein from Arabidopsis amounts to 74%, the similarity to the amino acid positions 1 to 316 of the TWD protein from Arabidopsis is 85,3%.